IN THE CLAIMS:

Cancel claims 4 and 11-14 without prejudice or disclaimer.

Please amend the claims and add new claims 20 and 21 as shown below:

Claim 1 (withdrawn): An isolated polynucleotide from coryneform bacteria, comprising an elongated sequence coding for 1-phosphofructokinase and/or 6-phosphofructokinase, wherein said sequence is elongated in front of the start codon and behind the stop codon of the gene, in each instance by up to about 700 base-pairs.

Claim 2 (withdrawn): The isolated polynucleotide according to Claim 1, wherein the elongated amino-acid sequence is represented by SEQ ID NO: 3 for the 1-phosphofructokinase gene and by SEQ ID NO: 1 for the 6-phosphofructokinase gene and the elongation in comparison with the sequence known from the state of the art consisting in SEQ ID NO: 3 of base-pairs 1 to 508 and 1684 to 2234 and in SEQ ID NO: 1 of base-pairs 1 to 531 and 1621 to 2160.

Claim 3 (currently amended): A process for the fermentative preparation of L-amino acids in coryneform bacteria, comprising:

a) fermenting the coryneform bacteria ~~producing the desired L-amino acid~~, in which at least the Corynebacterium glutamicum gene encoding ~~coding for 6-phosphofructokinase and/or the gene coding for~~ 1-phosphofructokinase ~~are~~/is ~~attenuated~~ eliminated by a method of mutagenesis selected from the group consisting of insertion of at least one base pair, deletion of at least one base pair, and transition or transversion mutagenesis with incorporation of a nonsense mutation, in a medium and for a time suitable for the formation of the L-amino acids; and

b) accumulating the produced L-amino acids in medium or in the cells of the bacteria.

Claim 4 (canceled)

Claim 5 (currently amended): The method according to claim 4 3, further comprising:

c) isolating the L-amino acid.

Claim 6 (original): The method according to claim 5, wherein the medium includes a fermentation broth and constituents of the fermentation broth remain in the end product in some proportion of their original quantity.

Claim 7 (original): The method according to claim 5, wherein constituents of a biomass of the cells remain in the end product in some proportion of their original quantity.

Claim 8 (original): The method according to claim 3, wherein the L-amino acids are L-lysine.

Claims 9-14 (canceled)

Claim 15 (currently amended): The method according to claim 3, wherein the bacteria being fermented further comprise~~, at the same time, one or more genes which are enhanced; wherein the~~ one or more overexpressed genes ~~is/are~~ selected from the group consisting of:

the Coryneform glutamicum gene that encodes ~~lysC coding for a feedback-resistant~~ aspartate kinase,

the Coryneform glutamicum gene that encodes ~~dapA coding for~~ dihydrodipicolinate synthase,

the Coryneform glutamicum gene that encodes ~~gap coding for~~ glyceraldehyde-3-phosphate dehydrogenase,

the Coryneform glutamicum gene that encodes ~~pyc coding for~~ pyruvate carboxylase,

the Coryneform glutamicum gene that encodes ~~mqo coding for~~ malate:quinone oxidoreductase,

the Coryneform glutamicum gene that encodes ~~zwf coding for~~ glucose-6-phosphate dehydrogenase,

~~simultaneously~~ the Coryneform glutamicum gene that encodes a protein that exports ~~lysE coding for~~ lysine ~~export~~,

the Coryneform glutamicum gene that encodes ~~zwa1 coding for~~ the zwa1 protein,

the Coryneform glutamicum gene that encodes ~~tpi coding for~~ triosephosphate isomerase, and

the Coryneform glutamicum gene that encodes ~~pgk coding for~~ 3-phosphoglycerate kinase.

Claim 16 (currently amended): The method according to claim 3, wherein the bacteria being fermented further comprise~~, at the same time,~~ one or more genes, which are eliminated, ~~attenuated; wherein the one or more genes is/are~~ selected from the group consisting of:

the Corynebacterium glutamicum ~~pck~~ gene ~~coding for~~ that encodes phosphoenolpyruvate carboxykinase,

the Corynebacterium glutamicum ~~pgi~~ gene ~~coding for~~ that encodes glucose-6-phosphate isomerase,

the Corynebacterium glutamicum gene ~~poxB coding for~~ that encodes pyruvate oxidase,

the Corynebacterium glutamicum gene ~~fda coding for~~ that encodes fructose bisphosphate aldolase, and

the Corynebacterium glutamicum gene ~~zwa2 coding for~~ that encodes the zwa2 protein, and

wherein said elimination is achieved by a method of mutagenesis selected from the group consisting of insertion of at least one base pair, deletion of at least one base pair, and transition or transversion mutagenesis with incorporation of a nonsense mutation.

Claim 17 (currently amended): The method according to claim 3, wherein ~~micro-organisms~~ bacteria of the species Corynebacterium glutamicum are employed.

Claim 18 (withdrawn): A coryneform bacterium in which at least the gene coding for 6-phosphofructokinase and/or the gene coding for 1-phosphofructokinase are/is present in attenuated form.

Claim 19 (withdrawn): An escherichia coli strain DH5alphamcr/pXK99EmobpfkB (= DH5mcr/ pXK99EmobpfkB), deposited as DSM 14741.

Claim 20 (new): The method according to claim 3, wherein said Corynebacterium glutamicum gene encoding 1-phosphofructokinase is a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO: 4.

Claim 21 (new): The method according to claim 20, wherein said polynucleotide comprises the nucleotide sequence of nucleotides 609 to 1598 of SEQ ID NO: 3.